

RAW SEQUENCE LISTING

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Application Serial Number: 10/600,997A
Source: 1FW/b
Date Processed by STIC: 9/28/06

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IFW16

RAW SEQUENCE LISTING

DATE: 09/28/2006

PATENT APPLICATION: US/10/600,997A

TIME: 09:05:34

Input Set : A:\A-71608 (substitute).ST25.txt

Output Set: N:\CRF4\09282006\J600997A.raw

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3 <110> APPLICANT: Murphy, Kenneth
4      Watanabe, Norihiko
5      Murphy, Theresa
6      Yang, Jianfei
8 <120> TITLE OF INVENTION: BTLA Nucleic Acids (amended)
10 <130> FILE REFERENCE: A-71608
12 <140> CURRENT APPLICATION NUMBER: 10/600,997A
13 <141> CURRENT FILING DATE: 2003-06-20
15 <150> PRIOR APPLICATION NUMBER: US 60/390,653
16 <151> PRIOR FILING DATE: 2002-06-20
18 <150> PRIOR APPLICATION NUMBER: US 60/438,593
19 <151> PRIOR FILING DATE: 2003-01-06
21 <160> NUMBER OF SEQ ID NOS: 62
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 283
27 <212> TYPE: PRT
28 <213> ORGANISM: Mus musculus
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37      20      25      30
40 Gly Lys His Phe Ile Thr Val Thr Thr Phe Thr Ser Ala Gly Asn Ile
41      35      40      45
44 Gly Glu Asp Gly Thr Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
45      50      55      60
48 Asn Gly Ile Val Ile Gln Trp Leu Lys Glu Gly Ile Lys Gly Leu Val
49 65      70      75      80
52 His Glu Phe Lys Glu Gly Lys Asp Asp Leu Ser Gln Gln His Glu Met
53      85      90      95
56 Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Val Val Gly Asn
57      100     105     110
60 Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
61      115     120     125
64 Thr Cys Tyr Ile Arg Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
65      130     135     140
68 Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Ile Asn Val Asp Tyr Asn
69 145     150     155     160
72 Ala Ser Ser Glu Ser Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
73      165     170     175
76 Pro Thr Val Ala Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
77      180     185     190

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81      195      200      205
84 Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
85      210      215      220
88 Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
89 225      230      235      240
92 Thr Asp Ser Glu Val Lys Arg Arg Ser Gln Leu Gln Leu Leu Asn Ser
93      245      250      255
96 Gly Pro Ser Pro Cys Val Phe Ser Ser Ala Phe Ala Ala Gly Trp Ala
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101      275      280
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105 <211> LENGTH: 282
106 <212> TYPE: PRT
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116      20      25      30
119 Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
120      35      40      45
123 Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
124      50      55      60
127 Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
128 65      70      75      80
131 His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
132      85      90      95
135 Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
136      100      105      110
139 Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
140      115      120      125
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144      130      135      140
147 Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn
148 145      150      155      160
151 Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
152      165      170      175
155 Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
156      180      185      190
159 Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
160      195      200      205
163 Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
164      210      215      220
167 Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
168 225      230      235      240
171 Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
172      245      250      255

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179 Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys
180                275                280
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184 <211> LENGTH: 852
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186 <213> ORGANISM: Mus musculus
188 <400> SEQUENCE: 3
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191 ggggccatcg cactcatcat tggctttggc atttcaggca agcacttcat cacggtcacg      120
193 accttcacct cagctggaaa cattggagag gacgggaccc tgagctgcac ttttgaacct      180
195 gacatcaaac tcaacggcat cgtcatccag tggctgaaag aaggcatcaa aggtttggct      240
197 cagagttca aagaaggcaa agacgacctc tcacagcagc atgagatgtt cagaggccgc      300
199 acagcagtgt ttgctgatca ggtggtagtt ggcaatgctt ccctgagact gaaaaacgtg      360
201 cagctcacgg atgctggcac ctacacatgt tacatccgca cctcaaaagg caaagggaat      420
203 gcaaacctag agtataagac cggagccttc agtatgccag agataaatgt ggactataat      480
205 gccagttcag agagtttacg ctgcgaggct cctcggtggt tccccagcc cacagtggcc      540
207 tgggcatctc aagtcgacca aggagccaac ttctcagaag tctcgaacac cagctttgag      600
209 ttgaactctg agaatgtgac catgaaggct gtatctgtgc tctacaatgt cacaatcaac      660
211 aacacatact cctgtatgat tgaaaatgac attgccaaag ccactgggga catcaaagt      720
213 acagattcag aggtcaaaag gcggagtcag ctgcagctgc tcaactccgg gccttccccg      780
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217 atgctaagat ga                                     852
220 <210> SEQ ID NO: 4
221 <211> LENGTH: 849
222 <212> TYPE: DNA
223 <213> ORGANISM: Homo sapiens
225 <400> SEQUENCE: 4
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230 actgtgcct cagctgggaa cattggggag gatggaatcc tgagctgcac ttttgaacct      180
232 gacatcaaac tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggtttggct      240
234 catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt cagaggccgg      300
236 acagcagtgt ttgctgatca agtgatagtt ggcaatgcct ctttgcggct gaaaaacgtg      360
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240 gctaaccttg agtataaaac tggagccttc agcatgccgg aagtgaatgt ggactataat      480
242 gccagctcag agaccttgcg gtgtgaggct ccccgatggt tccccagcc cacagtggct      540
244 tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac cagctttgag      600
246 ctgaactctg agaatgtgac catgaagggt gtgtctgtgc tctacaatgt tacgatcaac      660
248 aacacatact cctgtatgat tgaaaatgac attgccaaag caacagggga tatcaaagt      720
250 acagaatcgg agatcaaaag gcggagtcac ctacagctgc taaactcaa ggcttctctg      780
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257 <210> SEQ ID NO: 5
258 <211> LENGTH: 306
259 <212> TYPE: PRT
260 <213> ORGANISM: Mus musculus
262 <400> SEQUENCE: 5

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264 Met Lys Thr Val Pro Ala Met Leu Gly Thr Pro Arg Leu Phe Arg Glu
265 1 5 10 15
268 Phe Phe Ile Leu His Leu Gly Leu Trp Ser Ile Leu Cys Glu Lys Ala
269 20 25 30
272 Thr Lys Arg Asn Asp Glu Glu Cys Glu Val Gln Leu Asn Ile Lys Arg
273 35 40 45
276 Asn Ser Lys His Ser Ala Trp Thr Gly Glu Leu Phe Lys Ile Glu Cys
277 50 55 60
280 Pro Val Lys Tyr Cys Val His Arg Pro Asn Val Thr Trp Cys Lys His
281 65 70 75 80
284 Asn Gly Thr Ile Trp Val Pro Leu Glu Val Gly Pro Gln Leu Tyr Thr
285 85 90 95
288 Ser Trp Glu Glu Asn Arg Ser Val Pro Val Phe Val Leu His Phe Lys
289 100 105 110
292 Pro Ile His Leu Ser Asp Asn Gly Ser Tyr Ser Cys Ser Thr Asn Phe
293 115 120 125
296 Asn Ser Gln Val Ile Asn Ser His Ser Val Thr Ile His Val Arg Glu
297 130 135 140
300 Arg Thr Gln Asn Ser Ser Glu His Pro Leu Ile Thr Val Ser Asp Ile
301 145 150 155 160
304 Pro Asp Ala Thr Asn Ala Ser Gly Pro Ser Thr Met Glu Glu Arg Pro
305 165 170 175
308 Gly Arg Thr Trp Leu Leu Tyr Thr Leu Leu Pro Leu Gly Ala Leu Leu
309 180 185 190
312 Leu Leu Leu Ala Cys Val Cys Leu Leu Cys Phe Leu Lys Arg Ile Gln
313 195 200 205
316 Gly Lys Glu Lys Lys Pro Ser Asp Leu Ala Gly Arg Asp Thr Asn Leu
317 210 215 220
320 Val Asp Ile Pro Ala Ser Ser Arg Thr Asn His Gln Ala Leu Pro Ser
321 225 230 235 240
324 Gly Thr Gly Ile Tyr Asp Asn Asp Pro Trp Ser Ser Met Gln Asp Glu
325 245 250 255
328 Ser Glu Leu Thr Ile Ser Leu Gln Ser Glu Arg Asn Asn Gln Gly Ile
329 260 265 270
332 Val Tyr Ala Ser Leu Asn His Cys Val Ile Gly Arg Asn Pro Arg Gln
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336 Glu Asn Asn Met Gln Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val
337 290 295 300
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344 <210> SEQ ID NO: 6
345 <211> LENGTH: 289
346 <212> TYPE: PRT
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349 <400> SEQUENCE: 6
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355 Phe Phe Leu Ile Pro Tyr Leu Asp Ile Trp Asn Ile His Gly Lys Glu
356 20 25 30

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359 Ser Cys Asp Val Gln Leu Tyr Ile Lys Arg Gln Ser Glu His Ser Ile
360          35          40          45
363 Leu Ala Gly Asp Pro Phe Glu Leu Glu Cys Pro Val Lys Tyr Cys Ala
364          50          55          60
367 Asn Arg Pro His Val Thr Trp Cys Lys Leu Asn Gly Thr Thr Cys Val
368 65          70          75          80
371 Lys Leu Glu Asp Arg Gln Thr Ser Trp Lys Glu Glu Lys Asn Ile Ser
372          85          90          95
375 Phe Phe Ile Leu His Phe Glu Pro Val Leu Pro Asn Asp Asn Gly Ser
376          100          105          110
379 Tyr Arg Cys Ser Ala Asn Phe Gln Ser Asn Leu Ile Glu Ser His Ser
380          115          120          125
383 Thr Thr Leu Tyr Val Thr Asp Val Lys Ser Ala Ser Glu Arg Pro Ser
384          130          135          140
387 Lys Asp Glu Met Ala Ser Arg Pro Trp Leu Leu Tyr Ser Leu Leu Pro
388 145          150          155          160
391 Leu Gly Gly Leu Pro Leu Leu Ile Thr Thr Cys Phe Cys Leu Phe Cys
392          165          170          175
395 Cys Leu Arg Arg His Gln Gly Lys Gln Asn Glu Leu Ser Asp Thr Ala
396          180          185          190
399 Gly Arg Glu Ile Asn Leu Val Asp Ala His Leu Lys Ser Glu Gln Thr
400          195          200          205
403 Glu Ala Ser Thr Arg Gln Asn Ser Gln Val Leu Leu Ser Glu Thr Gly
404          210          215          220
407 Ile Tyr Asp Asn Asp Pro Asp Leu Cys Phe Arg Met Gln Glu Gly Ser
408 225          230          235          240
411 Glu Val Tyr Ser Asn Pro Cys Leu Glu Glu Asn Lys Pro Gly Ile Val
412          245          250          255
415 Tyr Ala Ser Leu Asn His Ser Val Ile Gly Leu Asn Ser Arg Leu Ala
416          260          265          270
419 Arg Asn Val Lys Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val Arg
420          275          280          285
423 Ser

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427 <210> SEQ ID NO: 7

428 <211> LENGTH: 870

429 <212> TYPE: DNA

430 <213> ORGANISM: Homo sapiens

432 <400> SEQUENCE: 7

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433 atgaagacat tgccctgccat gcttggaaact gggaaattat tttgggtctt cttcttaatc      60
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437 aagagacaat ctgaacactc catcttagca ggagatccct ttgaactaga atgccctgtg      180
439 aaatactgtg ctaacaggcc tcatgtgact tgggtgcaagc tcaatggaac aacatgtgta      240
441 aaacttgaag atagacaaac aagttggaag gaagagaaga acatttcatt tttcattcta      300
443 cattttgaac caatgcttcc taatgacaat gggtcatacc gctgttctgc aaattttcag      360
445 tctaattctca ttgaaagcca ctcaacaact ctttatgtga cagatgtaaa aggtgcctca      420
447 gaacgaccct ccaaggacga agtggcaagc agaccctggc tcctgtatag tttacttcc      480
449 ttgggggggat tgccctctact catcactacc tgggttctgcc tgttctgctg cctgagaagg      540
451 caccaaggaa agcaaaatga actctctgac acagcaggaa gggaaattaa tctggttgat      600
453 gctcacctta agagcgagca aacagaagca agcaccaggc aaaattccca agtactgcta      660

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VERIFICATION SUMMARY

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